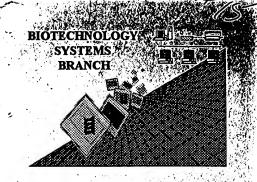# RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

16X1
7/22
DRAPER

Application Serial Number: 08/586,594C

Art Unit / Team No.: 1646

Date Processed by STIC: 7/23/98

THE ATTACHED PRINTOUT EXPLAINS THE **ERRORS DETECTED.**

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

| **ERROR DETECTED** | **SUGGESTED CORRECTION** | SERIAL NUMBER: 08/586,594C |

1 ✓____ Wrapped Nucleics

The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos

The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length

The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

4 _____ Misaligned Amino Acid
Numbering

The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

5 ✓ Non-ASCII

This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length

Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

7 _____ Wrong Designation

Sequence(s) _____ contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

8 _____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of N's or Xaa's
(NEW RULES)

Use of N's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

11 _____ Use of <213>Organism
(NEW RULES)

Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature
(NEW RULES)

Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"

13 _____ Wrong Format

File submitted was in the alphabetical heading format of the Old Sequence Rules.This is invalid since the
"Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Disclosures"
Federal Register Notice, Vol. 63, No. 104, Jun 1, 1998, p. 29620
applies to applications filed on or after July 1, 1998.

14 _____ OTHER _____

Draper

1646

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/586,594C*

DATE: 07/23/98
TIME: 09:24:21

INPUT SET: S27599.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

Does Not Comply
Corrected Diskette Needed

All item #5
on Error Summary Sheet

```
 1                              SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5      (i) APPLICANT: Friedman, Jeffrey M.
 6                    Lee, Gwo-Hua
 7                    Proenca, Ricardo
 8
 9     (ii) TITLE OF INVENTION: DB, THE RECEPTOR FOR LEPTIN, NUCLEIC
10              ACIDS ENCODING THE RECEPTOR, AND USES THEREOF
11
12    (iii) NUMBER OF SEQUENCES: 56
13
14     (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: David A. Jackson, Esq.
16           (B) STREET: 411 Hackensack Ave, Continental Plaza, 4th
17                   Floor
18           (C) CITY: Hackensack
19           (D) STATE: New Jersey
20           (E) COUNTRY: USA
21           (F) ZIP: 07601
22
23      (v) COMPUTER READABLE FORM:
24           (A) MEDIUM TYPE: Floppy disk
25           (B) COMPUTER: IBM PC compatible
26           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28
29     (vi) CURRENT APPLICATION DATA:
30           (A) APPLICATION NUMBER: US 08/586,594
31           (B) FILING DATE:
32           (C) CLASSIFICATION:
33
34   (viii) ATTORNEY/AGENT INFORMATION:
35           (A) NAME: Jackson Esq., David A.
36           (B) REGISTRATION NUMBER: 26,742
37           (C) REFERENCE/DOCKET NUMBER: 600-1-162
38
39     (ix) TELECOMMUNICATION INFORMATION:
40           (A) TELEPHONE: 201-487-5800
41           (B) TELEFAX: 201-343-1684
42
43
```

ERRORED SEQUENCES FOLLOW:

INPUT SET: S27599.raw

```
44    (2) INFORMATION FOR SEQ ID NO:1:
45
46        (i) SEQUENCE CHARACTERISTICS:
47            (A) LENGTH: 2529 base pairs
48            (B) TYPE: nucleic acid
49            (C) STRANDEDNESS: double
50            (D) TOPOLOGY: linear
51
52        (ii) MOLECULE TYPE: cDNA
53
54       (iii) HYPOTHETICAL: NO
55
56        (iv) ANTI-SENSE: NO
57
58
59       (vii) IMMEDIATE SOURCE:
60            (B) CLONE: A15 (OB-Ra)
61
62
63
64        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66    GGGCTCAGGT CGGCGTCGTA CCAGCCGCTG AAGCGGTTCT CCAGGTTCCA
67    GGCGCTCTCG        60
68
69    CCATGCCGGA TCAGCACCAG CTTGTAGCTC GTGCCGAATT CGGCACGAGG
70    TTGCTTTGGG       120
71
72    AATGAGCAAG GTCAAAACTG CTCTGCACTC ACAGACAACA CTGAAGGGAA
73    GACACTGGCT       180
74
75    TCAGTAGTGA AGGCTTCAGT TTTTCGCCAG CTAGGTGTAA ACTGGGACAT
76    AGAGTGCTGG       240
77
78    ATGAAAGGGG ACTTGACATT ATTCATCTGT CATATGGAGC CATTACCTAA
79    GAACCCCTTC       300
80
81    AAGAATTATG ACTCTAAGGT CCATCTTTTA TATGATCTGC CTGAAGTCAT
82    AGATGATTCG       360
83
84    CCTCTGCCCC CACTGAAAGA CAGCTTTCAG ACTGTCCAAT GCAACTGCAG
85    TCTTCGGGGA       420
86
87    TGTGAATGTC ATGTGCCGGT ACCCAGAGCC AAACTCAACT ACGCTCTTCT
88    GATGTATTTG       480
89
90    GAAATCACAT CTGCCGGTGT GAGTTTTCAG TCACCTCTGA TGTCACTGCA
91    GCCCATGCTT       540
92
93    GTTGTGAAAC CCGATCCACC CTTAGGTTTG CATATGGAAG TCACAGATGA
94    TGGTAATTTA       600
95
96    AAGATTTCTT GGGACAGCCA AACAATGGCA CCATTTCCGC TTCAATATCA
```

(handwritten notes in right margin):

This error appears throughout listing. Due to size of listing, only this page shown as a sample.

(See item #1 on Error summary sheet)

format error

→60
→120
→180